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(54) **PEPTIDE OR ARRANGEMENT OF PEPTIDES FORMING A STAPHYLOCOCCUS AUREUS EPITOPE BINDING SITE**

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CPC . *A61K 38/00*; *A61K 2039/505*; *A61K 39/00*; *C07K 16/1271*; *C07K 2319/00*; *C07K 16/1214*
See application file for complete search history.

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

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§ 371 (c)(1),

(2) Date: **Mar. 21, 2014**

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(87) PCT Pub. No.: **WO2013/041707**

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(65) **Prior Publication Data**

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(30) **Foreign Application Priority Data**

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A61K 47/00 (2006.01)

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C12P 21/08 (2006.01)

C07K 16/00 (2006.01)

C07K 16/12 (2006.01)

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(52) **U.S. Cl.**

CPC *C07K 16/1271* (2013.01); *G01N 33/56938* (2013.01); *A61K 38/00* (2013.01); *A61K 39/00*

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(57) **ABSTRACT**

The invention concerns a peptide or arrangement of peptides forming a *Staphylococcus aureus* epitope binding site comprising a first amino acid sequence and a second amino acid sequence, wherein the first amino acid sequence is at least 88% identical to sequence SEQ ID NO:1 and wherein the second amino acid sequence is at least 88% identical to sequence SEQ ID NO: 2.

20 Claims, 5 Drawing Sheets

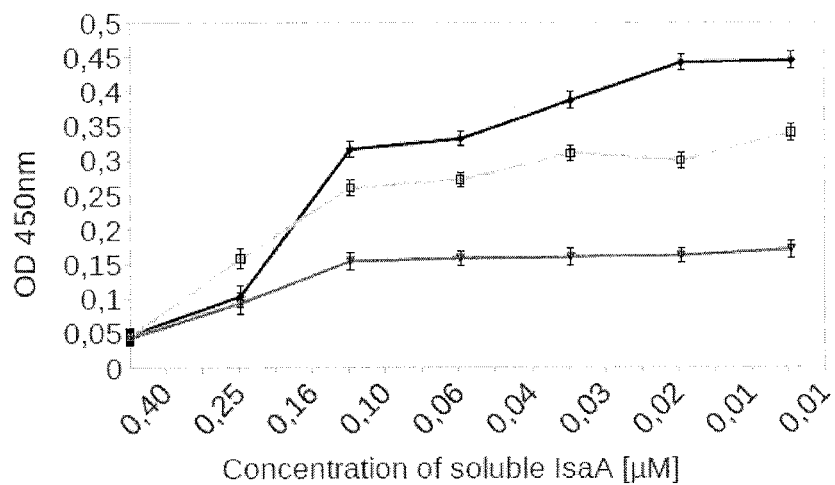


Fig. 1

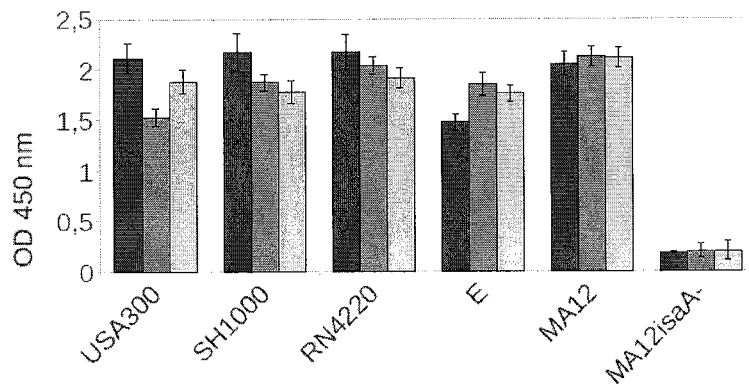


Fig. 2

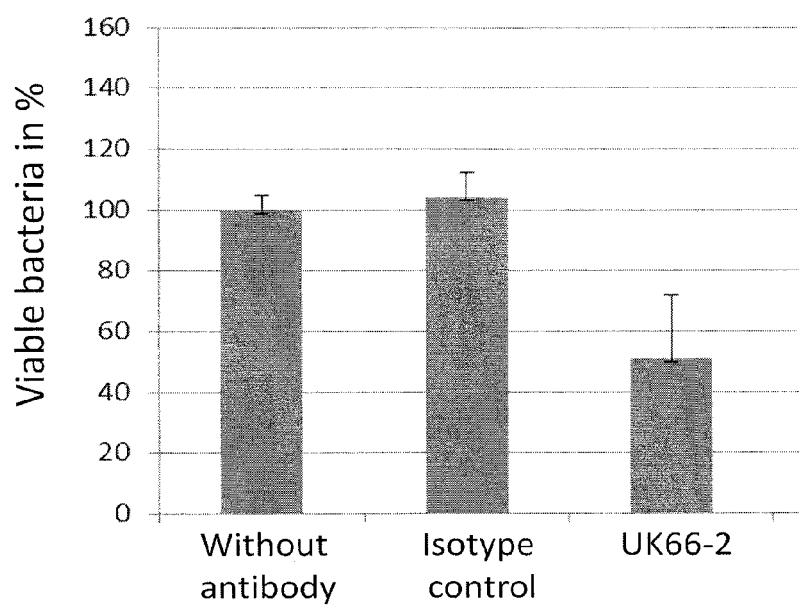


Fig. 3

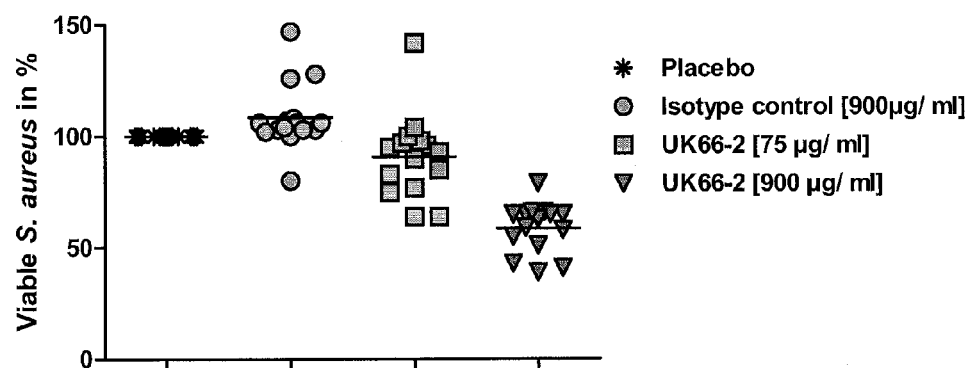


Fig. 4

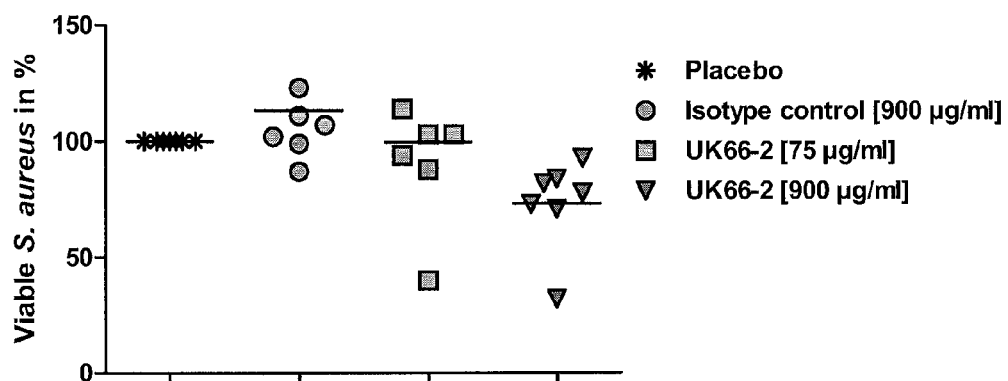


Fig. 5

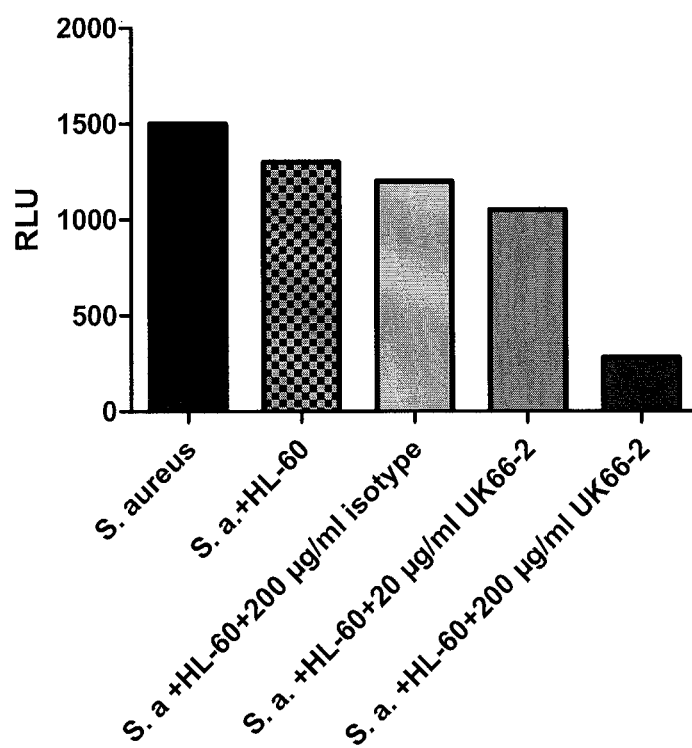


Fig. 6

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**PEPTIDE OR ARRANGEMENT OF PEPTIDES
FORMING A *STAPHYLOCOCCUS AUREUS*
EPITOPE BINDING SITE**

**CROSS REFERENCE TO RELATED
APPLICATIONS**

This application is the National Phase of PCT/EP2012/068703 filed on Sep. 21, 2012, which claims priority under 35 U.S.C. §119(e) to U.S. Provisional Application No. 61/545,763 filed on Oct. 11, 2011, under 35 U.S.C. §119(a) to patent application Ser. No. 11/182,598.0 filed in Europe on Sep. 23, 2011, all of which are hereby expressly incorporated by reference into the present application.

The invention concerns a peptide or arrangement of peptides forming a *Staphylococcus aureus* (= *S. aureus*) epitope binding site, a kit containing this peptide or arrangement of peptides, a use of this peptide or arrangement of peptides, a cell line which produces antibodies comprising this peptide or arrangement of peptides and a method of treatment.

From WO 2010/133600 A1 antibodies or fragments thereof directed against an *S. aureus* epitope of IsaA are known. These antibodies have a binding site formed by a heavy chain with a first variable region and a light chain with a second variable region wherein the sequence of the first variable region may be SEQ ID NO:13 and the sequence of the second variable region may be SEQ ID NO:14. The effectiveness of antibodies vis-à-vis *S. aureus* in a mammal depends on killing of *S. aureus* by phagocytosis by phagocytizing blood cells. The antibodies known from WO 2010/133600 A1 accelerated the phagocytosis process. After 30

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sequence is at least 88% identical to sequence SEQ ID NO:1 and the second amino acid sequence is at least 88% identical to SEQ ID NO:2.

In an embodiment the first amino acid sequence is at least 90% identical, in particular at least 92.5% identical, in particular at least 95% identical, in particular at least 97.5% identical, in particular 100% identical, to sequence SEQ ID NO:1. The second amino acid sequence is at least 90% identical, in particular at least 92.5% identical, in particular at least 95% identical, in particular at least 97.5% identical, in particular 100% identical, to sequence SEQ ID NO:2.

The first amino acid sequence may be part of the heavy chain and/or the second amino acid sequence may be part of the light chain of an antibody or antibody fragment. In this case the first amino acid sequence and the second amino acid sequence form the variable region of the antibody or antibody fragment. The binding site can also be formed by a single chain variable fragment. In this case the first amino acid sequence and the second amino acid sequence are comprised by a single chain variable fragment (scFv) or by a single chain variable fragment comprising an Fc fragment of an antibody (scFvFc). The Fc fragment enhances phagocytosis of *S. aureus* to which the scFvFc has bound.

The inventors modified the binding region of one of the antibodies known from WO 2010/133600 A1 and thereby developed a binding site that is more effective in support of killing of *S. aureus* by phagocytosis by phagocytizing blood cells in heparinized human whole blood than the known antibody. As can be seen from the following alignment sequence SEQ ID NO:1 differs in 17 from 118 amino acids from the corresponding sequence SEQ ID NO:13 and SEQ ID NO:2 differs in 8 from 113 amino acids from SEQ ID NO:14 known from WO 2010/133600 A1:

SEQ ID NO: 1	EVQLLESQGGGLVQPGGSLRLSCAASGFTFSNYMSWVRQAPGKGLEWVSDINGNGGSTYY	60
	V L ESGGGLV GGS L LSC ASGFTFSNYMSWVRQ P K L E V DINGNGGSTYY	
SEQ ID NO: 13	MADVKLVESGGGLVKLGSLKLSASGFTFSNYMSWVRQTPEKRLVLADINGNGGSTYY	62
SEQ ID NO: 1	PDTVKGRTISRDN SKNTLYLQMN SLRAEDTAVYVCVRGGYALDYWGQGT TVTVSS	118
	PDTVKGRTISRDN KNTLYLQ M SL EDTA YYCVRGGYALDYWGQGT TVTVSS	
SEQ ID NO: 13	PDTVKGRTISRDN AKNTLYLQMS LKSEDTALYYCVRGGYALDYWGQGT TVTVSS	120
SEQ ID NO: 2	DVVMQTPLSLSVTPGPASISCRSSQSLVHNGNTYLHWYLQKPGQSPQLLIYRVSNRF	60
	DVVMQTPLSL V G ASISCRSSQSLVHNGNTYLHWYLQKPGQSP LLIYRVSNRF	
SEQ ID NO: 14	DVVMQTPLSLPVS LGDQASISCRSSQSLVHNGNTYLHWYLQKPGQSPKLLIYRVSNRF	60
SEQ ID NO: 2	SGVPDRFSGSGSGTDFTLKISRVEAEDG VYYCSQSTHPVPTFGGGTKLELKR	113
	SGVPDRFSGSGSGTDFTLKISRVEAED G VY CSQSTHPVPTFGGGTKLELKR	
SEQ ID NO: 14	SGVPDRFSGSGSGTDFTLKISRVEAEDLG VYFCSQSTHPVPTFGGGTKLELKR	113

minutes of incubation the killing of *S. aureus* by human neutrophils in the presence of the antibodies specific for an epitope of IsaA has been enhanced by about 25% to 30% compared to an unspecific control antibody.

The object of the present invention is to provide a *S. aureus* epitope binding site that is very effective in an antibody or fragment of antibody with respect to the killing of *S. aureus* by phagocytizing blood cells and therefore is well suited for a treatment of infections caused by *Staphylococcus aureus*. Furthermore, the binding site should be well suited for a detection of *S. aureus*. A further object of the present invention is to provide a kit containing the binding site, a use of the binding site, a cell line secreting antibodies, antibody fragments, ScFvs or ScFvFc comprising the binding site and a method of treatment.

According to the invention a peptide or arrangement of peptides forming a *Staphylococcus aureus* epitope binding site comprising a first amino acid sequence and a second amino acid sequence is provided. The first amino acid

Identical amino acids are displayed in the interspace between the sequences.

Antibodies containing the variable region comprising the first amino acid sequence and the second amino acid sequence exhibit high affinity to the immunodominant structure IsaA in methicillin resistant and methicillin sensitive *S. aureus* and a high specificity with respect to the binding to this structure.

The antibody may be a monoclonal antibody, in particular an antibody of the IgG type, in particular of the IgG1 type, the IgG2 type, or the IgG4 type. The fragment may be an Fab fragment, Fab/c fragment, Fv fragment, Fab' fragment or F(ab')₂ fragment. These fragments are particularly useful for the detection of *S. aureus* because the cell wall of *S. aureus* contains protein A which unspecifically binds immunoglobulins via their Fc-parts.

In an embodiment of the invention the antibody is a recombinant antibody produced in cells of a cell line, in particular an insect cell line or a mammalian cell line, in particular a Chinese hamster ovary (CHO) cell line or a hybridoma cell

line. The part of the antibody which is not formed by the first amino acid sequence and the second amino acid sequence is at least 85% identical, in particular at least 90% identical, in particular at least 92.5% identical, in particular at least 95% identical, in particular at least 97.5% identical, in particular 100% identical, to the corresponding part of a human antibody. The light chain of the antibody can comprise sequence SEQ ID NO:6, in particular sequence SEQ ID NO:7 and the heavy chain can comprise the sequence SEQ ID NO:4, in particular SEQ ID NO:5, sequence SEQ ID NO:9, in particular sequence SEQ ID NO:10, or sequence SEQ ID NO:11, in particular SEQ ID NO:12. Sequences SEQ ID NO:7, SEQ ID NO:5, SEQ ID NO:10 and SEQ ID NO:12 comprise the leader sequence SEQ ID NO:8 which is from the MOPC 63, Ig kappa chain V-III of KV3A9_{mouse}. This leader sequence enables a good expression in mammalian cells. The sequence SEQ ID NO:4 comprises sequence SEQ ID NO:1 and an IgG1 heavy chain, human γ 1 allotype Gm 1,17. Sequence SEQ ID NO:6 comprises sequence SEQ ID NO:2 and the IgG light chain K. Sequence SEQ ID NO:9 comprises sequence SEQ ID NO:1 and the IgG2 heavy chain, allotype G2m(23). Sequence SEQ ID NO:11 comprises SEQ ID NO:1 and an IgG4 heavy chain.

The peptide or arrangement of peptides according to the invention may be used as a medicament. Especially they may be used as a medicament for the treatment of a human being or an animal which human being or animal has an infection with *S. aureus*, especially methicillin resistant or methicillin sensitive *S. aureus*, or is at risk of getting such an infection. The treatment in the sense of this invention comprises prophylaxis. The animal may be a mammal. The human being or the animal may have a mastitis, an *S. aureus* bacteremia, in particular a primary or secondary bacteremia, a blood stream infection, in particular a primary or secondary blood stream infection, a prosthetic infection, a graft infection, a soft tissue infection, a surgery associated infection, an infant or newborn infection, a dialysis associated infection, a pneumonia, a bone infection, or a sepsis caused by the infection. The mastitis may be a bovine mastitis. If a cow has bovine mastitis no useable milk is produced by the cow and if the cow is treated with antibiotics as it is usual in this case the milk produced by this cow has to be discarded until no antibiotics are contained in the milk of this cow. This disadvantage of the usual treatment may be avoided by use of the peptide or arrangement of peptides according to the invention as a medicament for the treatment of the bovine mastitis.

The peptide or arrangement of peptides may be present in mixture with at least one other peptide or arrangement of peptides directed against at least one further epitope of *S. aureus*. This further epitope may be located on the antigen on which the epitope is located, i. e. IsaA, or on a further antigen. The use of such a mixture as a medicament may be more efficient than the use of a medicament which solely contains the peptide or arrangement of peptides according to the invention. This may be owing to the high variability of *S. aureus* that causes different extents of expression of the antigens on different strains such that more bacteria are recognized by the mixture of antibodies or fragments than by the antibodies or fragments alone.

The peptide or arrangement of peptides can be present in a mixture with at least one antibiotic. In the human being or animal to be treated with the medicament mutated *S. aureus* may be present in addition to common *S. aureus*. The mutated *S. aureus* may have mutated IsaA that cannot be recognized by the peptide or arrangement of peptides according to the invention. In this case the antibiotic may be effective against the mutated *S. aureus*.

The peptide or arrangement of peptides according to the invention may be present in a mixture with plasma or blood of a mammal, especially a human being. The inventors found that the peptide or arrangement of peptides according to the invention mixed with plasma may be much more effective than the peptide or arrangement of peptides according to the invention contained in a saline solution.

The medicament may be a medicament that is prepared for systemic and/or local application. The inventors have recognized that the treatment of a severe *S. aureus* infection with the peptide or arrangement of peptides according to the invention results in a significant reduction of the mortality rates and number of *S. aureus* in the organs of the treated human being or animal.

The invention also concerns a kit containing the peptide or arrangement of peptides according to the invention for the detection, especially a highly specific detection, of *S. aureus*.

The invention further concerns the use of the peptide or arrangement of peptides according to the invention for a detection, especially a highly specific detection, of *S. aureus*.

Furthermore, the invention concerns a cell line, in particular an insect cell line or a mammalian cell line, in particular a Chinese hamster ovary (CHO) cell line or a hybridoma cell line, which produces an antibody, antibody fragment, ScFv or ScFvFc as specified above.

The invention further concerns a method of treatment of a human being or an animal which human being or animal has an infection with *Staphylococcus aureus*, especially methicillin resistant or methicillin sensitive *Staphylococcus aureus*, or is at risk of getting such an infection, wherein the peptide or arrangement of peptides according to the invention is administered to the human being or the animal. The peptide or arrangement of peptides is administered in a dosage that is sufficient to reduce the amount of *S. aureus* or to cause an elimination of *S. aureus* in the human being or the animal. The peptide or arrangement of peptides may be mixed with a suitable carrier.

The human being or the animal may have mastitis, an *S. aureus* bacteremia, in particular a primary or secondary bacteremia, a blood stream infection, in particular a primary or secondary blood stream infection, a prosthetic infection, a graft infection, a soft tissue infection, a surgery associated infection, an infant or newborn infection, a dialysis associated infection, a pneumonia, a bone infection, or a sepsis caused by the infection.

The peptide or arrangement of peptides may be present in a mixture with at least one other peptide or arrangement of peptides directed against at least one further epitope of *S. aureus*. The peptide or arrangement of peptides may be mixed with plasma or blood of a mammal, especially of a human being, before it is administered. The peptide or arrangement of peptides may be administered topically or systemically, in particular intravenously, intrapulmonary, intraperitoneally, nasally or sublingually. They may also be administered together with at least one antibiotic.

EMBODIMENTS OF THE INVENTION

FIG. 1 shows the result of a competitive ELISA to determine binding of different anti-IsaA antibodies to the IsaA antigen.

FIG. 2 shows a bacterial cell ELISA to determine binding of different anti-IsaA antibodies to different *S. aureus* strains.

FIG. 3 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood.

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FIG. 4 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood from healthy blood donors (n=15).

FIG. 5 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood from dialysis patients.

FIG. 6 shows the opsonophagocytic killing of bioluminescent *S. aureus* strain Newman (Newlux) in the presence of two concentrations of anti-IsaA antibody UK66-2 versus isotype control in HL-60 cells.

ScFv molecules containing sequences SEQ ID NOs:1 and 2, SEQ ID NOs:1 and 3 as well as other sequences have been expressed in *E. coli* and tested for binding and affinity in ELISA and competitive ELISA. The results showed that affinity of an ScFv molecule containing sequences SEQ ID NO:1 and SEQ ID NO:2 is about 10 times higher than affinity of an ScFv molecule containing sequences SEQ ID NO:1 and SEQ ID NO:3.

Vector constructs for the expression of complete antibodies has been transfected in CHO cells. IgG1 heavy chain, human $\gamma 1$ allotype Gm1,17 according to sequence SEQ ID NO:4 (comprising sequence SEQ ID NO:1) with the Igk leader sequence SEQ ID NO:8 (resulting in sequence SEQ ID NO:5) and IgG light chain K according to SEQ ID NO:6 (comprising sequence SEQ ID NO:2) with the Igk leader sequence SEQ ID NO:8 (resulting in sequence SEQ ID NO:7) have been expressed to form antibody UK66-2. To investigate the influence of the isotype on functional activity IgG2 and IgG4 isotypes have been synthesized.

For this the IgG1 heavy chain has been replaced by IgG2 heavy chain, allotype G2m (23) according to sequence SEQ ID NO:9 with the Igk leader sequence SEQ ID NO:8 (resulting in sequence SEQ ID NO:10) or IgG4 heavy chain according to sequence SEQ ID NO:11 with the Igk leader sequence SEQ ID NO:8 (resulting in sequence SEQ ID NO:12).

After expression IgG1 antibodies have been purified from the supernatant of the CHO cells via a protein A column. The purified antibodies have been tested for the kinetics of binding, binding in ELISA, competitive ELISA, Western Blot and immunofluorescence und for function in phagocytosis assays with human phagocytizing blood cells. In funktional assays the antibody comprising sequences SEQ ID NOs:1 and 2 (UK66-2) enhanced oxidative burst und killing of *S. aureus* significantly more than known antibody UK66.

The kinetics of binding of IsaA to immobilized antibody UK66-2 was determined by means of label-free surface plasmon resonance using the BIACORE®2000 system (GE Healthcare Europe GmbH, Munzinger Strasse 5, 79111 Freiburg, Germany). Reversible immobilization of the antibody UK66-2 was performed using an anti Fab antibody. Interaction analyses were performed using HBS-EP buffer (10 mM HEPES pH 7.4, 150 mM NaCl, 3.4 mM EDTA, 0.005% Tween 20 (polyoxyethylene (20) sorbitan monolaurate)). Sensorgrams were recorded at a flow rate of 30 μ l/min at 25° C.

Affinities and rate constants for association (k_{on}) and for dissociation (k_{off}) were calculated using the BIA evaluation software 4.0.1 (Biacore) fitting the obtained sensorgrams to a 1:1 Langmuir binding model. In this way a dissociation constant K_D of 4.8 nM was determined in two independent measurements. Rate constants for association and dissociation of the interaction between UK66-2 and IsaA were determined to be $3.7 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$ (k_{on}) and $1.8 \times 10^{-3} \text{ s}^{-1}$ (k_{off}), respectively.

FIG. 1 shows the result of a competitive ELISA to determine binding of different anti-IsaA antibodies to soluble recombinant IsaA antigen. The optical density at 450 nm

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indicates binding of the antibodies to IsaA. Soluble IsaA was added in different concentrations. The three lines represent the results received with the following anti IsaA antibodies:

Upper line at 0.01 μ M soluble IsaA: UK66 (reference antibody known from WO 2010/133600 A1)

Middle line at 0.01 μ M soluble IsaA: UK66-2 (antibody with a binding site comprising sequences SEQ ID NO:1 and SEQ ID NO:2)

Lower line at 0.01 μ M soluble IsaA: UK66-3 (antibody with a binding site comprising sequences SEQ ID NO:1 and SEQ ID NO:3)

Method Description:

Nunc-Maxisorp 96-well plates were coated with 50 μ l/well of IsaA (0.5 μ g/well in 1xPBS) and incubated at 4° C. overnight. The next day the plates were washed three times with PBS pH 7.4 containing 0.05% Tween 20 (polyoxyethylene (20) sorbitan monolaurate) (PBST). After washing blocking was performed by addition of 200 μ l 5% skimmed milk powder/PBS and incubated for 1 h at room temperature. The wells were washed twice with PBST (0.05%) and primary anti-IsaA antibody was added in serial concentrations ranging from 0.4 μ M to 0.01 μ M. The primary anti-IsaA-IgG1 antibodies were diluted in 2.5% skimmed milk powder/PBS and incubated for 1 h at 37° C. The wells were then washed three times with PBST (0.05%) and 50 μ l of horseradish peroxidase linked secondary antibody 1:5000 diluted in 2.5% skimmed milk powder/PBS was added and incubated for 1 h at 37° C. The wells were washed with PBST (0.05%) four times and 50 μ l of TMB (3,3',5,5'-tetramethylbenzidine) (Thermo Scientific Pierce ELISA substrate) was added and incubated for 15 min at 37° C. The reaction was stopped with 100 μ l of 1N H_2SO_4 and optical density of the substrate reaction was analyzed with an ELISA plate reader at OD 450 nm.

FIG. 2 shows a bacterial cell ELISA to determine binding of different anti-IsaA antibodies to the *S. aureus* strains USA300, SH1000, RN4220, E, MA12 and MA12isaA-. In MA12isaA- the immunodominant structure IsaA has been deleted. The optical density at 450 nm indicates binding of the antibodies to bacterial cells. The three columns represent the results received with the following anti IsaA antibodies:

Left column: antibody UK66 (reference antibody)

Middle column: antibody UK66-2

Right column: antibody UK66-3.

Method Description:

The strains of *S. aureus* were cultured in B media at 37° C. overnight. The bacteria were pelleted by centrifugation at 13000 rpm for 1 minute and washed with PBS (phosphate buffered saline). After the centrifugation step the pellet was resuspended in 1 ml PBS. A bacteria suspension containing 5×10^7 bacteria/50 μ l was prepared. Nunc-Maxisorp 96-well plates were coated with 50 μ l/well of the bacteria suspension and incubated at 4° C. overnight. The next day the plates were washed three times with PBS pH 7.4 containing 0.05% Tween 20 (polyoxyethylene (20) sorbitan monolaurate) (PBST). After washing blocking was performed by addition of 200 μ l 5% skimmed milk powder/PBS and incubated for 1 h at room temperature. The wells were washed twice with PBST (0.05%) and primary anti-IsaA antibody was added. The primary anti-IsaA-IgG1 antibodies were diluted 1:2000 in 2.5% skimmed milk powder/PBS and 50 μ l/well were added and incubated for 1 h at 37° C. The wells were then washed three times with PBST (0.05%) and 50 μ l of horseradish peroxidase linked secondary antibody 1:5000 diluted in 2.5% skimmed milk powder/PBS was added and incubated for 1 h at 37° C. The wells were washed with PBST (0.05%) four times and 50 μ l of TMB (3,3',5,5'-tetramethylbenzidine) (Thermo Scientific Pierce ELISA substrate) was added and incubated for 15

min at 37° C. The reaction was stopped with 100 µl of 1N H₂SO₄ and optical density of the substrate reaction was analyzed with an ELISA plate reader at OD 450 nm.

FIG. 3 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood. Bacteria were incubated 30 min with the heparinized human whole blood. The number of viable bacteria after incubation without antibody solution was set 100% (left column). Killing was significantly increased in the presence of UK66-2 (right column) compared to isotype control antibodies (middle column).

Method Description:

S. aureus strain Newman was cultured in LB medium at 37° C. overnight. The bacteria were pelleted by centrifugation at 13000 rpm for 1 minute and washed with PBS. The centrifugation step was repeated and the bacteria were resuspended in 1 ml PBS. Bacteria solution of 5×10⁷ bacteria/20 µl was prepared. 100 µl of heparinized blood was added into 1.5 ml tubes and stored on ice. 20 µl of bacterial suspension and antibody solution were added, excluded the negative control sample which contained bacteria but no antibodies. The samples were incubated at 37° C. for 30 min with constant movement overhead in a hybridisation oven. Phagocytosis was stopped by placing the samples on ice. Blood cells were lysed with 0.1% fresh prepared Saponin (20 min on ice). Two serial dilutions of the samples were prepared. 20 µl of 10⁻², 10⁻³ and 10⁻⁴ dilution, respectively were plated in duplicate on LB plates and incubated at 37° C. for 24 h. The colonies were counted and killing was calculated setting the number of viable bacteria in blood without antibody solution as 100%.

FIG. 4 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood from healthy blood donors (n=15). FIG. 5 shows the quantification of killing of *S. aureus* strain Newman by phagocytosis by phagocytizing blood cells in heparinized human whole blood from dialysis patients (n=7). In both cases bacteria were incubated 60 min with the heparinized blood. The number of viable bacteria after incubation without antibody solution was set 100% (left scatter plot "Placebo"). Killing was significantly increased in the presence of UK66-2 (third and fourth scatter plot "UK66-2 [75 µg/ml]" and "UK66-2[900 µg/ml]") compared to isotype control antibodies (second scatter plot "Isotype control [900 µg/ml]").

Method Description:

S. aureus strain Newman was cultured in LB medium at 37° C. overnight. The bacteria were pelleted by centrifugation at 13000 rpm for 1 minute and washed with PBS. The centrifugation step was repeated and the bacteria were resuspended in 1 ml PBS. Bacteria solution of 5×10⁷ bacteria/20 µl was prepared. 100 µl of heparinized blood was added into 1.5 ml tubes and stored on ice. 20 µl of bacterial suspension and

antibody solution were added, excluded the negative control sample which contained bacteria but no antibodies. The samples were incubated at 37° C. for 60 min with constant movement overhead in a hybridisation oven. Phagocytosis was stopped by placing the samples on ice. Blood cells were lysed with 0.1% fresh prepared Saponin (20 min on ice). Two serial dilutions of the samples were prepared. 20 µl of 10⁻², 10⁻³ and 10⁻⁴ dilution, respectively were plated in duplicate on LB plates and incubated at 37° C. for 24 h. The colonies were counted and killing was calculated. The number of viable bacteria in blood without antibody solution was set 100%.

FIG. 6 shows killing of bioluminescent *S. aureus* (S. a.) strain Newman (Newlux) in the presence of two concentrations of anti-IsaA antibody UK66-2 (20 µg/ml and 200 µg/ml versus isotype control (200 µg/ml) in HL-60 cells. Determination of relative number of surviving bacteria was performed by measurement of bioluminescence. Surviving bacteria are given as light emission (RLU=relative light units). Bacterial killing is concentration dependent with UK66-2 and is not observed with an isotype-matched human IgG1 control antibody.

Method Description:

A single colony of *S. aureus* strain Newman harbouring the luxABCE operon was used to inoculate 5 ml LB medium. Since the luxABCE operon causes a luminescence in living but not in dead bacteria the luminescence correlates with the number of living bacteria. The bacteria were cultivated overnight and 50 µl of this culture were used to inoculate 5 ml LB medium supplemented with 30 µg/ml kanamycin. The culture was cultivated on a rotary shaker at 200 rpm for 4-6 h at 37° C. Bioluminescence of the bacteria was determined using a Lumat LB 9501 luminometer (Berthold Technologies, Bad Wildbad, Germany). The culture was ready for performing the assay when 100 µl of the culture generated bioluminescence signals ranged between 16000-24000 relative light units (RLU). Following cultivation, the bacteria were washed twice in phosphate buffered saline (PBS) and resuspended in Opti-MEM® medium (Life Technologies, Darmstadt, Germany) to a final concentration of 1×10⁶/ml. Phagocytic HL-60 cells were differentiated with 0.8% DMF for 5 days and resuspended to 1×10⁸ cells/ml in Opti-MEM®, and 50 µl per well were seeded in a 96-well tissue culture plate (Greiner Bio-One, Frickenhausen, Germany). Antibody solution (50 µl) was added followed by 100 µl of *S. aureus* (1×10⁹/ml). HL-60 cells, antibody and bacteria were incubated at 37° C. and bioluminescence was measured continuously at 15 min intervals for 240 min to determine the optimal signal-noise ratio. All assays were performed in triplicate and repeated at least three times. Bioluminescence was determined using the multi-mode reader Infinite 200 Pro (TECAN, Mannedorf, Switzerland).

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 14

<210> SEQ ID NO 1

<211> LENGTH: 118

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Modified sequence of a sequence from mus musculus

<400> SEQUENCE: 1

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
 Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Arg Gly Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 115

<210> SEQ ID NO 2
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Modified sequence of a sequence from mus
 musculus

<400> SEQUENCE: 2

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ile
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
 100 105 110

Arg

<210> SEQ ID NO 3
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Modified sequence of a sequence from mus
 musculus

<400> SEQUENCE: 3

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln Ser Leu Val His Ile
 20 25 30
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 35 40 45
 Pro Arg Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Ile Pro

-continued

50	55	60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile		
65	70	75 80
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Ser Gln Ser		
	85	90 95
Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys		
	100	105 110

Arg

<210> SEQ ID NO 4
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Sequence containing SEQ ID NO:1 and IgG1 heavy chain, human gammal allotype Gm1,17

<400> SEQUENCE: 4

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr		
	20	25 30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
	35	40 45
Ser Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val		
	50	55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
	65	70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90 95
Val Arg Arg Gly Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr		
	100	105 110
Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
	115	120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
	130	135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
	145	150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
	165	170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
	180	185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
	195	200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
	210	215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser		
	225	230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
	245	250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
	260	265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
	275	280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		

-continued

290	295	300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
305	310	315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
	325	330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		
	340	345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys		
	355	360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
	370	375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
	385	390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser		
	405	410 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
	420	425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	435	440 445

<210> SEQ ID NO 5
 <211> LENGTH: 468
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: SEQ ID NO:4 with leader sequence SEQ ID NO:8
 <400> SEQUENCE: 5

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
1	5 10 15
Gly Ser Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val	
	20 25 30
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr	
	35 40 45
Phe Ser Asn Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	
	50 55 60
Leu Glu Trp Val Ser Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr	
	65 70 75 80
Pro Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys	
	85 90 95
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala	
	100 105 110
Val Tyr Tyr Cys Val Arg Arg Gly Gly Tyr Tyr Ala Leu Asp Tyr Trp	
	115 120 125
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
	130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	
	145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
	165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
	180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
	195 200 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	

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210	215	220
His Lys Pro Ser Asn Thr	Lys Val Asp Lys Lys Val Glu Pro Lys Ser	
225	230	235 240
Cys Asp Lys Thr His Thr	Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
	245	250 255
Gly Gly Pro Ser Val Phe	Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
	260	265 270
Met Ile Ser Arg Thr Pro	Glu Val Thr Cys Val Val Val Asp Val Ser	
	275	280 285
His Glu Asp Pro Glu Val	Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
	290	295 300
Val His Asn Ala Lys Thr	Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
305	310	315 320
Tyr Arg Val Val Ser Val	Leu Thr Val Leu His Gln Asp Trp Leu Asn	
	325	330 335
Gly Lys Glu Tyr Lys Cys	Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
	340	345 350
Ile Glu Lys Thr Ile Ser	Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
	355	360 365
Val Tyr Thr Leu Pro Pro	Ser Arg Asp Glu Leu Thr Lys Asn Gln Val	
	370	375 380
Ser Leu Thr Cys Leu Val	Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
385	390	395 400
Glu Trp Glu Ser Asn Gly	Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
	405	410 415
Pro Val Leu Asp Ser Asp	Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
	420	425 430
Val Asp Lys Ser Arg Trp	Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
	435	440 445
Met His Glu Ala Leu His	Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
450	455	460
Ser Pro Gly Lys		
465		
<210> SEQ ID NO 6		
<211> LENGTH: 219		
<212> TYPE: PRT		
<213> ORGANISM: Artificial		
<220> FEATURE:		
<223> OTHER INFORMATION: SEQ ID NO:2 with human IgG light chain K		
<400> SEQUENCE: 6		
Asp Val Val Met Thr Gln Thr	Pro Leu Ser Leu Ser Val Thr Pro Gly	
1	5	10 15
Gln Pro Ala Ser Ile Ser	Cys Arg Ser Ser Gln Ser Leu Val His Ile	
	20	25 30
Asn Gly Asn Thr Tyr Leu His	Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
	35	40 45
Pro Gln Leu Leu Ile Tyr	Arg Val Ser Asn Arg Phe Ser Gly Val Pro	
	50	55 60
Asp Arg Phe Ser Gly Ser	Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65	70	75 80
Ser Arg Val Glu Ala Glu	Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser	
	85	90 95
Thr His Val Pro Trp Thr	Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys	

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100					105					110					
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
		115						120						125	
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	130							135					140		
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
	145					150					155				160
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165						170				175	
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180						185					190	
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
		195						200					205		
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
	210						215								

<210> SEQ ID NO 7

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: SEQ ID NO:6 with leader sequence SEQ ID NO:8

<400> SEQUENCE: 7

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser
			20					25					30		
Val	Thr	Pro	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser
			35				40					45			
Leu	Val	His	Ile	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Arg	Val	Ser	Asn	Arg	Phe
	65				70					75				80	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
			100					105					110		
Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120						125		
Leu	Glu	Leu	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	130					135						140			
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
	145				150					155					160
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
			165						170					175	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		180						185					190		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		195					200						205		
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	210					215					220				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
	225					230					235				

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<210> SEQ ID NO 8
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 8

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly
 20

<210> SEQ ID NO 9
 <211> LENGTH: 444
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: SEQ ID NO:1 with IgG2 heavy chain, allotype G2m
 (23)

<400> SEQUENCE: 9

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Arg Arg Gly Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
 210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
 225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
 260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr

-continued

290	295	300
Val Val His Gln Asp Trp	Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
305	310	315 320
Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr		
	325 330 335	
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg		
	340 345 350	
Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly		
	355 360 365	
Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro		
	370 375 380	
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser		
	385 390 395 400	
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln		
	405 410 415	
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His		
	420 425 430	
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	435 440	

<210> SEQ ID NO 10
 <211> LENGTH: 464
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: SEQ ID NO:9 with leader sequence SEQ ID NO:8
 <400> SEQUENCE: 10

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
1	5 10 15
Gly Ser Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val	
	20 25 30
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr	
	35 40 45
Phe Ser Asn Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	
	50 55 60
Leu Glu Trp Val Ser Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr	
	65 70 75 80
Pro Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys	
	85 90 95
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala	
	100 105 110
Val Tyr Tyr Cys Val Arg Arg Gly Gly Tyr Tyr Ala Leu Asp Tyr Trp	
	115 120 125
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
	130 135 140
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr	
	145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
	165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
	180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
	195 200 205
Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp	

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210	215	220
His Lys Pro Ser Asn Thr	Lys Val Asp Lys Thr	Val Glu Arg Lys Cys
225	230	235 240
Cys Val Glu Cys Pro Pro	Cys Pro Ala Pro Pro	Val Ala Gly Pro Ser
	245	250 255
Val Phe Leu Phe Pro Pro	Lys Pro Lys Asp Thr	Leu Met Ile Ser Arg
	260	265 270
Thr Pro Glu Val Thr Cys	Val Val Val Asp Val	Ser His Glu Asp Pro
	275	280 285
Glu Val Gln Phe Asn Trp	Tyr Val Asp Gly Val	Glu Val His Asn Ala
	290	295 300
Lys Thr Lys Pro Arg Glu	Glu Gln Phe Asn Ser	Thr Phe Arg Val Val
	305	310 315 320
Ser Val Leu Thr Val Val	His Gln Asp Trp Leu	Asn Gly Lys Glu Tyr
	325	330 335
Lys Cys Lys Val Ser Asn	Lys Gly Leu Pro Ala	Pro Ile Glu Lys Thr
	340	345 350
Ile Ser Lys Thr Lys Gly	Gln Pro Arg Glu Pro	Gln Val Tyr Thr Leu
	355	360 365
Pro Pro Ser Arg Glu Glu	Met Thr Lys Asn Gln	Val Ser Leu Thr Cys
	370	375 380
Leu Val Lys Gly Phe Tyr	Pro Ser Asp Ile Ser	Val Glu Trp Glu Ser
	385	390 395 400
Asn Gly Gln Pro Glu Asn	Asn Tyr Lys Thr Thr	Pro Pro Met Leu Asp
	405	410 415
Ser Asp Gly Ser Phe Phe	Leu Tyr Ser Lys Leu	Thr Val Asp Lys Ser
	420	425 430
Arg Trp Gln Gln Gly Asn	Val Phe Ser Cys Ser	Val Met His Glu Ala
	435	440 445
Leu His Asn His Tyr Thr	Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys
	450	455 460
<210> SEQ ID NO 11		
<211> LENGTH: 445		
<212> TYPE: PRT		
<213> ORGANISM: Artificial		
<220> FEATURE:		
<223> OTHER INFORMATION: SEQ ID NO:1 with IgG4 heavy chain		
<400> SEQUENCE: 11		
Glu Val Gln Leu Leu Glu	Ser Gly Gly Gly Leu Val	Gln Pro Gly Gly
1	5	10 15
Ser Leu Arg Leu Ser Cys	Ala Ala Ser Gly Phe Thr	Phe Ser Asn Tyr
	20	25 30
Tyr Met Ser Trp Val Arg	Gln Ala Pro Gly Lys Gly	Leu Glu Trp Val
	35	40 45
Ser Asp Ile Asn Gly Asn	Gly Gly Ser Thr Tyr Tyr	Pro Asp Thr Val
	50	55 60
Lys Gly Arg Phe Thr Ile	Ser Arg Asp Asn Ser	Lys Asn Thr Leu Tyr
	65	70 75 80
Leu Gln Met Asn Ser Leu	Arg Ala Glu Asp Thr	Ala Val Tyr Tyr Cys
	85	90 95
Val Arg Arg Gly Gly Tyr	Tyr Ala Leu Asp Tyr Trp	Gly Gln Gly Thr
	100	105 110
Thr Val Thr Val Ser Ser	Ala Ser Thr Lys Gly	Pro Ser Val Phe Pro

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115	120	125
Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly 130 135 140		
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn 145 150 155 160		
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln 165 170 175		
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser 180 185 190		
Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser 195 200 205		
Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys 210 215 220		
Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu 225 230 235 240		
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu 245 250 255		
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln 260 265 270		
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys 275 280 285		
Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu 290 295 300		
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys 305 310 315 320		
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys 325 330 335		
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser 340 345 350		
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 355 360 365		
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln 370 375 380		
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly 385 390 395 400		
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln 405 410 415		
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn 420 425 430		
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys 435 440 445		
<210> SEQ ID NO 12		
<211> LENGTH: 465		
<212> TYPE: PRT		
<213> ORGANISM: Artificial		
<220> FEATURE:		
<223> OTHER INFORMATION: SEQ ID NO:11 with leader sequence SEQ ID NO:8		
<400> SEQUENCE: 12		
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro 1 5 10 15		
Gly Ser Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val 20 25 30		
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr 35 40 45		

Phe 50	Asn	Tyr	Tyr	Met	Ser 55	Trp	Val	Arg	Gln	Ala 60	Pro	Gly	Lys	Gly
Leu 65	Glu	Trp	Val	Ser 70	Asp	Ile	Asn	Gly	Asn	Gly 75	Gly	Ser	Thr	Tyr 80
Pro	Asp	Thr	Val	Lys 85	Gly	Arg	Phe	Thr	Ile 90	Ser	Arg	Asp	Asn	Ser 95
Asn	Thr	Leu	Tyr 100	Leu	Gln	Met	Asn	Ser 105	Leu	Arg	Ala	Glu	Asp 110	Thr
Val	Tyr	Tyr	Cys 115	Val	Arg	Arg	Gly 120	Gly	Tyr	Tyr	Ala	Leu 125	Asp	Tyr
Gly	Gln	Gly	Thr 130	Thr	Val	Thr 135	Val	Ser	Ser	Ala	Ser 140	Thr	Lys	Gly
Ser 145	Val	Phe	Pro	Leu	Ala 150	Pro	Cys	Ser	Arg	Ser 155	Thr	Ser	Glu	Ser
Ala	Ala	Leu	Gly 165	Cys	Leu	Val	Lys	Asp	Tyr 170	Phe	Pro	Glu	Pro	Val
Val	Ser	Trp	Asn 180	Ser	Gly	Ala	Leu	Thr 185	Ser	Gly	Val	His	Thr 190	Phe
Ala	Val	Leu	Gln 195	Ser	Ser	Gly	Leu 200	Tyr	Ser	Leu	Ser	Ser 205	Val	Val
Val	Pro	Ser	Ser 210	Ser	Leu	Gly 215	Thr	Lys	Thr	Tyr	Thr 220	Cys	Asn	Val
His 225	Lys	Pro	Ser	Asn	Thr 230	Lys	Val	Asp	Lys	Arg 235	Val	Glu	Ser	Lys
Gly	Pro	Pro	Cys 245	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly
Ser	Val	Phe	Leu 260	Phe	Pro	Pro	Lys	Pro 265	Lys	Asp	Thr	Leu	Met 270	Ile
Arg	Thr	Pro	Glu 275	Val	Thr	Cys	Val 280	Val	Val	Asp	Val	Ser 285	Gln	Glu
Pro	Glu	Val	Gln 290	Phe	Asn	Trp 295	Tyr	Val	Asp	Gly	Val 300	Glu	Val	His
Ala 305	Lys	Thr	Lys	Pro	Arg 310	Glu	Glu	Gln	Phe	Asn 315	Ser	Thr	Tyr	Arg
Val	Ser	Val	Leu 325	Thr	Val	Leu	His	Gln	Asp 330	Trp	Leu	Asn	Gly	Lys
Tyr	Lys	Cys	Lys 340	Val	Ser	Asn	Lys	Gly 345	Leu	Pro	Ser	Ser	Ile 350	Glu
Thr	Ile	Ser	Lys 355	Ala	Lys	Gly	Gln 360	Pro	Arg	Glu	Pro	Gln 365	Val	Tyr
Leu 370	Pro	Pro	Ser	Gln	Glu	Glu 375	Met	Thr	Lys	Asn	Gln 380	Val	Ser	Leu
Cys 385	Leu	Val	Lys	Gly	Phe 390	Tyr	Pro	Ser	Asp	Ile 395	Ala	Val	Glu	Trp
Ser	Asn	Gly	Gln 405	Pro	Glu	Asn	Asn	Tyr	Lys	Thr 410	Thr	Pro	Pro	Val
Asp	Ser	Asp	Gly 420	Ser	Phe	Phe	Leu	Tyr 425	Ser	Arg	Leu	Thr	Val 430	Asp
Ser	Arg	Trp	Gln 435	Glu	Gly	Asn	Val 440	Phe	Ser	Cys	Ser	Val 445	Met	His
Ala 450	Leu	His	Asn	His	Tyr	Thr 455	Gln	Lys	Ser	Leu	Ser	Leu 460	Ser	Leu

-continued

Lys
465

<210> SEQ ID NO 13
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<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 13

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Asn Tyr Tyr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu
           35           40           45
Leu Val Ala Asp Ile Asn Gly Asn Gly Gly Ser Thr Tyr Tyr Pro Asp
           50           55           60
Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65           70           75           80
Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Tyr
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Gly Thr Thr Val Thr Val Ser Ser
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<210> SEQ ID NO 14
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<400> SEQUENCE: 14

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           20           25           30
Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
           35           40           45
Pro Lys Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
           50           55           60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
           85           90           95
Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
           100          105          110

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Arg

The invention claimed is:

1. An antibody or antigen binding fragment, comprising:
a variable heavy chain sequence comprising SEQ ID NO: 1; and
a variable light chain sequence comprising SEQ ID NO: 2;
wherein said antibody or antigen binding fragment specifically binds to an epitope of *Staphylococcus aureus*.
2. The antibody or antigen binding fragment of claim 1,
wherein the antibody or antigen binding fragment enables killing of *Staphylococcus aureus* by promoting phagocytosis by blood cells in a subject.

3. The antibody or antigen binding fragment of claim 1, wherein the heavy chain and/or the light chain are comprised by a single chain variable fragment (scFv) or by a single chain variable fragment comprising an Fc fragment of an antibody (scFvFc).

4. The antibody or antigen binding fragment of claim 1, wherein the antibody or antigen binding fragment is a monoclonal antibody.

5. The antibody or antigen binding fragment of claim 1, wherein the fragment is an Fab fragment, Fab/c fragment, Fv fragment, Fab' fragment or F(ab')₂ fragment.

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6. The antibody or antigen binding fragment of claim 1, wherein the antibody or antigen binding fragment is a recombinant antibody produced in cells of a cell line.

7. The antibody or antigen binding fragment of claim 1, wherein the light chain comprises sequence SEQ ID NO:6, and the heavy chain comprises sequence SEQ ID NO:4, sequence SEQ ID NO:9, or sequence SEQ ID NO:11.

8. The antibody or antigen binding fragment of claim 1 suitable for use as a medicament.

9. The antibody or antigen binding fragment of claim 8, wherein the medicament is a medicament for the treatment of a human being or an animal which human being or animal has an infection with *Staphylococcus aureus* or is at risk of getting such an infection.

10. The antibody or antigen binding fragment of claim 9, wherein the human being or the animal has a mastitis, an *S. aureus* bacteremia, a blood stream infection, a prosthetic infection, a graft infection, a soft tissue infection, a surgery associated infection, an infant or newborn infection, a dialysis associated infection, a pneumonia, a bone infection, or a sepsis caused by the infection.

11. The antibody or antigen binding fragment of claim 8, wherein the antibody or antigen binding fragment is present in a mixture with at least one other antibody or antigen binding fragment directed against at least one further epitope of *Staphylococcus aureus*.

12. The antibody or antigen binding fragment of claim 8, wherein the antibody or antigen binding fragment is present in a mixture with at least one antibiotic.

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13. The antibody or antigen binding fragment of claim 8, wherein the antibody or antigen binding fragment is present in a mixture with plasma or blood of a mammal.

14. The antibody or antigen binding fragment of claim 8, wherein the medicament is a medicament for systemic and/or local application.

15. Kit containing the antibody or antigen binding fragment of claim 1 for the detection of *Staphylococcus aureus*.

16. Method of treatment of a human being or an animal which human being or animal has an infection with *Staphylococcus aureus* or is at risk of getting such an infection, wherein the antibody or antigen binding fragment as claimed in claim 1 is administered to the human being or the animal.

17. Method according to claim 16, wherein the human being or the animal has a mastitis, an *S. aureus* bacteremia, a blood stream infection, a prosthetic infection, a graft infection, a soft tissue infection, a surgery associated infection, an infant or newborn infection, a dialysis associated infection, a pneumonia, a bone infection, or a sepsis caused by the infection.

18. Method as claimed in claim 16, wherein the antibody or antigen binding fragment is mixed with plasma or blood of a mammal before it is administered.

19. Method as claimed in claim 16, wherein the antibody or antigen binding fragment is administered topically or systemically.

20. Method as claimed in claim 16, wherein the antibody or antigen binding fragment is administered together with at least one antibiotic.

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